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#### RAW SEQUENCE LISTING PATENT APPLICATION US/08/790,757...

DATE: 12/18/96 TIME: 14:31:40 -

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This Raw Listing contains the General Information Section and up to the first 5 pages.

#### SEQUENCE LISTING 1 ENTERED 2 General Information: 3 (1) (i) APPLICANT: Ponath, Paul D. 5 Ringler, Douglas J. 6 Jones, S. Tarran 7 Newman, Walter 8 Saldanha, Jos 9 Bendig, Mary M. 10 (ii) TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH Á4 7 11 12 INTEGRIN 13 14 (iii) NUMBER OF SEQUENCES: 63 15 16 (iv) CORRESPONDENCE ADDRESS: (A) ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C. 17 18 (B) STREET: Two Militia Drive 19 (C) CITY: Lexington 20 (D) STATE: Massachusetts 21 (E) COUNTRY: USA 22 (F) ZIP: 02173 23 24 (V) COMPUTER READABLE FORM: 25 (A) MEDIUM TYPE: Floppy disk 26 (B) COMPUTER: IBM PC compatible 27 (C) OPERATING SYSTEM: PC-DOS/MS-DOS 28 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 29 30 (vi) CURRENT APPLICATION DATA: 31 (A) APPLICATION NUMBER: 08/700,737 32 (B) FILING DATE: 15-AUG-1996 33 . (C) CLASSIFICATION: 34 35 (VIII) ATTORNEY/AGENT INFORMATION: 36 (A) NAME: Brook, David E. 37 (B) REGISTRATION NUMBER: 22,592 38 (C) REFERENCE/DOCKET NUMBER: LKS95-10 39 40 (ix) TELECOMMUNICATION INFORMATION: 41 (A) TELEPHONE: (617) 861-6240 42 (B) TELEFAX: (617) 861-9540 43 44 45 (2) INFORMATION FOR SEQ ID NO:1:

# RAW SEQUENCE LISTING PATENT APPLICATION US/08/700,737

DATE: 12/18/96 TIME: 14:31:43

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7	THE PARTITION OF THE PA	
8	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 494 base pairs	
9	(B) TYPE: nucleic acid	
0	(C) STRANDEDNESS: double	•
1	(D) TOPOLOGY: linear	
52	(D) 10F0H001: 22.0000	
3	,	
54	•	
55	(ix) FEATURE:	
56 57	(A) NAME/KEY: CDS	
5 <i>1</i> 58	(B) LOCATION: 13444	
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61	770 TD VO.1.	
62	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:	
63	TO DETERMINE AMYVMONTON TOGTATCAAC AGCTACAAGT	60
64	TTACKRGWMK WCATGRRATG SASCTRKRTC ATYYTCTTCT TGGTATCAAC AGCTACAAGT	
65	GTCCACTCCC AGGTCCAACT GCAGCAGCCT GGGGCTGAGC TTGTGAAGCC TGGGACTTCA	120
66		
67	GTGAAGCTGT CCTGCAAGGG TTATGGCTAC ACCTTCACCA GCTACTGGAT GCACTGGGTG	180
68		
69	AAGCAGAGGC CTGGACAAGG CCTTGAGTGG ATCGGAGAGA TTGATCCTTC TGAGAGTAAT	240
70		
71	ACTAACTACA ATCAAAAATT CAAGGGCAAG GCCACATTGA CTGTAGACAT TTCCTCCAGC	300
72		360
73 74	ACAGCCTACA TGCAGCTCAG CAGCCTGACA TCTGAGGACT CTGCGGTCTA CTATTGTGCA	300
7 <del>4</del> 75		420
76	AGAGGGGGTT ACGACGGATG GGACTATGCT ATTGACTACT GGGGTCAAGG CACCTCAGTC	120
77		480
78	ACCGTCTCCT CAGCCAAAAC GACACCRYCN CSYKTMTMYC YYSBDNNCCC YKGRWSCYTG	
79		494
80	GNNGAAGCTT GGGA	
81	TO THE WOLL.	
82	(2) INFORMATION FOR SEQ ID NO:2:	
83	THE THE PART OF PARTIES !	
84	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 144 amino acids	
85	(B) TYPE: amino acid	
86	(C) STRANDEDNESS:	
87	(D) TOPOLOGY: linear	
88	(5) 1010101	
89 90		
91		
92		
93		
94	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:	
95		
96	Met Xaa Xaa Xaa Xaa Ile Xaa Phe Leu Val Ser Thr Ala Thr Ser	
97	1	
98	val His Ser Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Lys	
0.0	Val His Ser GIN val GIN Led GIN GIN The Table 1	

### RAW SEQUENCE LISTING PATENT APPLICATION US/08/700,737

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153	TAT	GGC	TAC	ACC	TTC	ACC	AGC	TAC	TGG	ATG	UAC	TGG	Val	I.vs	G]	Ln A	rq	
154	TAT Tyr	Glv	Tyr	Thr	Phe	Thr	Ser	Tyr	Trp	мет	HIS	E	Val		-		- 3	
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156	dom	CCA	CAA	GGC	CTT	GAG	TGG	ATC	GGA	GAG	ATT	GAI	CCT	TCI	. 0	1 6	er Zer	
157	CCI	GOA	Gln	Glv	CTT Leu	Glu	Trp	Ile	Gly	Glu	Ile	Asp	Pro	Sei	G.	Lu .	75	
158		GLY	01			65	_				70						13	
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164			maa	mcc	AGC	ACA	GCC	TAC	ATG	CAG	CTC	AGC	AGC	CT	G A	CA	TCT	330
165	GAC	ATT	TCC	200	AGC Ser	Thr	Ala	Tvr	Met	Glr	Lev	ı Ser	Ser	Le	u T	'nr	Ser	
166	Asp	116	Ser	Der	Ser			- 4	100					10	5			
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169	GAG	GAC	TCT	GCG	GTC Val	m	T.T.	Cvs	. Ala	Arc	Gly	, Gly	Ty:	: As	рG	:ly	Trp	
170	Glu	Asp			, var	Tyr	Lyr	115					120	)				
171			110					_			,							
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173	GAC	TA?	r GC7	' AT'	GAC	TAC	, TGC	, GG.	יונט י	Gl	v Th	r Se	r Va	l Th	r			
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232 233	CGAT	TACT	'AG T	CGAC	ATC	AAC	TTG	CCI	GTT	AGG	CTG	TTG	GTG Val	CTT	CTC	TTG Leu		51
233 234	CGAT	TACT	'AG T	CGAC	ATC Met	AAC Lys	Lev	Pro	GTT Val	AGG	CTG Lev	TTG Lev 145		CTT Leu	CTC Lev	TTG Leu		51
233 234 235					Met	Lys	140	Pro	val	. Arg	Per	145	,					
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233 234 235 236 237 238	TTC Phe 150	TGG Trp	ATT Ile	CCT Pro	GTT Val	TCC Ser 155	GGA Gly	GGT GCA	GAT Asp	GTT Val	GTG Val 160	145 GTG Val	ACT Thr	CAA Gln TCT	ACT Thr	CCA Pro 165		
233 234 235 236 237 238 239 240 241 242	TTC Phe 150	TGG Trp	ATT Ile	CCT Pro	GTT Val GTC Val	TCC Ser 155 AGC	140 GGA Gly	GGT GCA	GAT Asp	GTT Val	GTG Val 160	145 GTG Val	ACT Thr	CAA Gln TCT	ACT Thr	CCA Pro 165		99
233 234 235 236 237 238 239 240 241 242 243	TTC Phe 150 CTC Leu	TGG Trp TCC Ser	ATT Ile CTG Leu	CCT Pro CCT Pro	GTT Val GTC Val	TCC Ser 155 AGC Ser	GGA Gly TTT Phe	GGT Gly GGA Gly	GAT Asp GAT Asp	GTT Val CAA Gln 175	GTG Val 160 GTT Val	GTG Val TCT Ser	ACT Thr	CAA Gln TCT Ser	ACT Thr TGC Cys 180	CCA Pro 165 AGG Arg		99 147
233 234 235 236 237 238 239 240 241 242	TTC Phe 150 CTC Leu	TGG Trp TCC Ser	ATT Ile CTG Leu	CCT Pro	GTT Val GTC Val 170	TCC Ser 155 AGC Ser	GGA Gly TTT Phe	GGT GLy GGA GLY	GAT Asp GAT Asp	GTT Val CAA Gln 175	GTG Val 160 GTT Val	GTG Val TCT Ser	ACT Thr ATC Ile	CAA Gln TCT Ser	ACT Thr TGC Cys 180	CCA Pro 165 AGG Arg		99
233 234 235 236 237 238 239 240 241 242 243 244 245 246	TTC Phe 150 CTC Leu	TGG Trp TCC Ser	ATT Ile CTG Leu	CCT Pro CCT Pro AGT Ser	GTT Val GTC Val 170	TCC Ser 155 AGC Ser	GGA Gly TTT Phe	GGT GLY GGA GLY	GAT Asp GAT Asp	GTT Val CAA Gln 175	GTG Val 160 GTT Val	GTG Val TCT Ser	ACT Thr ATC Ile	CAA Gln TCT Ser	ACT Thr TGC Cys 180	CCA Pro 165 AGG Arg		99 147
233 234 235 236 237 238 239 240 241 242 243 244 245 246 247	TTC Phe 150 CTC Leu TCT Ser	TGG Trp TCC Ser AGT Ser	ATT Ile CTG Leu CAG Gln	CCT Pro CCT Pro AGT Ser 185	GTT Val GTC Val 170 CTT Leu	TCC Ser 155 AGC Ser GCA	GGA Gly TTT Phe	GGT GLY GGA GLY AGT Ser	GAT Asp GAT Asp TAT Tyr 190	GTT Val CAA Gln 175 GGG Gly	GTG Val 160 GTT Val AAC Asn	GTG Val TCT Ser	ACT Thr ATC Ile TAT	CAA Gln TCT Ser TTG Leu 195	ACT Thr TGC Cys 180 TCT Ser	CCA Pro 165 AGG Arg TGG		99 147 195
233 234 235 236 237 238 239 240 241 242 243 244 245 246	TTC Phe 150 CTC Leu TCT Ser	TGG Trp TCC Ser AGT Ser	ATT Ile CTG Leu CAG Gln	CCT Pro CCT Pro AGT Ser 185	GTT Val GTC Val 170 CTT Leu	TCC Ser 155 AGC Ser GCA Ala	GGA Gly TTT Phe	GGT Gly GGA Gly AGT Ser	GAT Asp GAT Asp TAT Tyr 190	GTT Val CAA Gln 175 GGG Gly	GTG Val 160 GTT Val AAC Asn	GTG Val TCT Ser	ACT Thr ATC Ile TAT Tyr	CAA Gln TCT Ser TTG Leu 195	ACT Thr TGC Cys 180 TCT Ser	CCA Pro 165 AGG Arg TGG Trp		99 147
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233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251	TTC Phe 150 CTC Leu TCT Ser TAC	TGG Trp TCC Ser AGT Ser CTG Leu	ATT Ile CTG Leu CAG Gln CAC His 200	CCT Pro CCT Pro AGT Ser 185 AAG Lys	GTT Val GTC Val 170 CTT Leu CCT Pro	TCC Ser 155 AGC Ser GCA Ala	GGA Gly TTT Phe AAG Lys	GGT GLY GGA GLY AGT Ser TCT Ser 205	GAT Asp GAT Asp TAT Tyr 190 CCA	GTT Val CAA Gln 175 GGG Gly CAG	GTG Val 160 GTT Val AAC Asn	GTG Val TCT Ser ACC Thr	ACT Thr ATC Ile TAT Tyr ATC Ile 210	CAA Gln TCT Ser TTG Leu 195 TAT	ACT Thr TGC Cys 180 TCT Ser GGG Gly	CCA Pro 165 AGG Arg TGG Trp		99 147 195 243
233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250	TTC Phe 150 CTC Leu TCT Ser TAC	TGG Trp TCC Ser AGT Ser CTG Leu	ATT Ile CTG Leu CAG Gln CAC His 200	CCT Pro CCT Pro AGT Ser 185 AAG Lys	GTT Val GTC Val 170 CTT Leu CCT	TCC Ser 155 AGC Ser GCA Ala	GGA Gly TTT Phe AAG Lys	GGT Gly GGA Gly AGT Ser TCT Ser	GAT Asp GAT Asp TAT Tyr 190 CCA Pro	GTT Val CAA Gln 175 GGG Gly CAG	GTG Val 160 GTT Val AAC Asn	GTG Val TCT Ser ACC Thr	ACT Thr ATC Ile TAT Tyr ATC Ile 210	CAA Gln TCT Ser TTG Leu 195 TAT Tyr	ACT Thr TGC Cys 180 TCT Ser GGG Gly	CCA Pro 165 AGG Arg TGG Trp		99 147 195
233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254	TTC Phe 150 CTC Leu TCT Ser TAC Tyr	TGG Trp TCC Ser AGT Ser CTG Leu AAC	ATT Ile CTG Leu CAG Gln CAC His 200 AGA Arg	CCT Pro CCT Pro AGT Ser 185 AAG Lys	GTT Val GTC Val 170 CTT Leu CCT	TCC Ser 155 AGC Ser GCA Ala	GGA Gly TTT Phe AAG Lys CAG Gln	GGT Gly GGA Gly AGT Ser TCT Ser 205 CCA	GAT Asp GAT Asp TAT Tyr 190 CCA Pro	GTT Val CAA Gln 175 GGG Gly CAG	GTG Val 160 GTT Val AAC Asn	GTG Val TCT Ser ACC Thr	ACT Thr ATC Ile TAT Tyr ATC Ile 210 GGC Gly	CAA Gln TCT Ser TTG Leu 195 TAT Tyr	ACT Thr TGC Cys 180 TCT Ser GGG Gly	CCA Pro 165 AGG Arg TGG Trp		99 147 195 243
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233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254	TTC Phe 150 CTC Leu TCT Ser TAC Tyr	TGG Trp TCC Ser AGT Ser CTG Leu AAC Asn 215	ATT Ile CTG Leu CAG Gln CAC His 200 AGA Arg	CCT Pro CCT Pro AGT Ser 185 AAG Lys	GTT Val GTC Val 170 CTT Leu CCT Pro	TCC Ser 155 AGC Ser GCA Ala GGC Gly	GGA Gly TTT Phe AAG Lys CAG Gln GTG Val	GGT Gly GGA Gly AGT Ser TCT Ser 205	GAT Asp GAT Tyr 190 CCA Pro	GTT Val  CAA Gln 175 GGG Gly  CAG Gln AGG Arg	GTG Val 160 GTT Val AAC Asn CTC Leu TTC	GTG Val TCT Ser ACC Thr CTC Leu AGT Ser 225	ACT Thr ATC Ile TAT Tyr ATC Ile 210 GGC Gly	CAA Gln TCT Ser TTG Leu 195 TAT Tyr	ACT Thr TGC Cys 180 TCT Ser GGG Gly	CCA Pro 165 AGG Arg TGG Trp		99 147 195 243